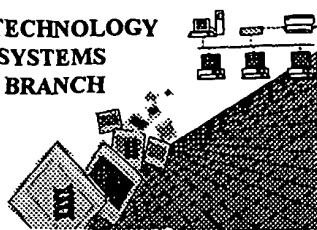# RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _____*10/053,645*_____

Source: _____*OIPE*_____

Date Processed by STIC: _____*2/7/2002*_____

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**
FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO **REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.1 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:
http://www.uspto.gov/web/offices/pac/checker

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.
Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<**http://www.uspto.gov/ebc/efs/downloads/documents.htm**> , **EFS Submission User Manual** - ePAVE)
2. **U.S. Postal Service:** U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202
3. **Hand Carry directly to:**
   U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7th Floor, Examiner Name, Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202
   Or
   U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. **Federal Express, United Parcel Service, or other delivery service to:** U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 01/29/2002

ERROR DETECTED   **SUGGESTED CORRECTION**   SERIAL NUMBER: *10/053,645*

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1____Wrapped Nucleics
Wrapped Aminos

The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2____Invalid Line Length

The rules require that a line not exceed 72 characters in length. This includes white spaces.

3____Misaligned Amino
Numbering

The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

4____Non-ASCII

The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

5____Variable Length

Sequence(s)____contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6____PatentIn 2.0
"bug"

A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.

7____Skipped Sequences
(OLD RULES)

Sequence(s) ____ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8____Skipped Sequences
(NEW RULES)

Sequence(s) ____ missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

9____Use of n's or Xaa's
(NEW RULES)

Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa; and which residue n or Xaa represents.

10____Invalid <213>
Response

Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence *(and more)*

11____Use of <220>

Sequence(s) *1-19* missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)

12____PatentIn 2.0
"bug"

Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13____Misuse of n

n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

AMC/MH – Biotechnology Systems Branch – 08/21/2001

OIPE

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/053,645

DATE: 02/07/2002
TIME: 12:30:12

Input Set : A:\SEQ LISTING OF 10412-022.TXT
Output Set: N:\CRF3\02072002\J053645.raw

*Does Not Comply
Corrected Diskette Needed*

```
  4 <110> APPLICANT: Robert E. Klem
  6 <120> TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING A
  7        CELL-PROLIFERATIVE DISORDER USING CRE DECOY OLIGOMERS, BCL-2
  8        ANTISENSE OLIGOMERS, AND HYBRID OLIGOMERS THEREOF
 11 <130> FILE REFERENCE: 10412-022-999
 13 <140> CURRENT APPLICATION NUMBER: US/10/053,645
 14 <141> CURRENT FILING DATE: 2002-01-22
 16 <150> PRIOR APPLICATION NUMBER: 60/263,244
 17 <151> PRIOR FILING DATE: 2001-01-22
 19 <160> NUMBER OF SEQ ID NOS: 43
 21 <170> SOFTWARE: FastSEQ for Windows Version 4.0
 23 <210> SEQ ID NO: 1
 24 <211> LENGTH: 20
 25 <212> TYPE: DNA
 26 <213> ORGANISM: Artificail sequence
 26 <220> FEATURE:
 26 <223> OTHER INFORMATION:
 28 <400> SEQUENCE: 1
 29 cagcgtgcgc catccttccc                                          20
 31 <210> SEQ ID NO: 2
 32 <211> LENGTH: 35
 33 <212> TYPE: DNA
 34 <213> ORGANISM: Artificail sequence
 36 <220> FEATURE:
 36 <223> OTHER INFORMATION:
 36 <400> SEQUENCE: 2
 37 cttttcctct gggaaggatg gcgcacgctg ggaga                         35
 39 <210> SEQ ID NO: 3
 40 <211> LENGTH: 20
 41 <212> TYPE: DNA
 42 <213> ORGANISM: Artificail sequence
 44 <220> FEATURE:
 44 <223> OTHER INFORMATION:
 44 <400> SEQUENCE: 3
 45 gatgcaccta cccagcctcc                                          20
 47 <210> SEQ ID NO: 4
 48 <211> LENGTH: 33
 49 <212> TYPE: DNA
 50 <213> ORGANISM: Artificail sequence
 52 <220> FEATURE:
 52 <223> OTHER INFORMATION:
 52 <400> SEQUENCE: 4
 53 acggggtacg gaggctgggt aggtgcatct ggt                           33
```

C--> 26
W--> 26
W--> 26
C--> 34
W--> 36
W--> 36
C--> 42
W--> 44
W--> 44
C--> 50
W--> 52
W--> 52

Artificial (global misspelling)
see item 11 on Erra Summary Sheet (global erra)

RAW SEQUENCE LISTING   DATE: 02/07/2002
PATENT APPLICATION: US/10/053,645   TIME: 12:30:12

Input Set : A:\SEQ LISTING OF 10412-022.TXT
Output Set: N:\CRF3\02072002\J053645.raw

```
       55 <210> SEQ ID NO: 5
       56 <211> LENGTH: 20
       57 <212> TYPE: DNA
C--> 58 <213> ORGANISM: Artificail sequence
W--> 60 <220> FEATURE:
W--> 60 <223> OTHER INFORMATION:
       60 <400> SEQUENCE: 5
       61 acaaaggcat cctgcagttg                              20
       63 <210> SEQ ID NO: 6
       64 <211> LENGTH: 36
       65 <212> TYPE: DNA
C--> 66 <213> ORGANISM: Artificail sequence
W--> 68 <220> FEATURE:
W--> 68 <223> OTHER INFORMATION:
       68 <400> SEQUENCE: 6
       69 cccccaactg caggatgcct ttgtggaact gtacgg          36
       71 <210> SEQ ID NO: 7
       72 <211> LENGTH: 20
       73 <212> TYPE: DNA
C--> 74 <213> ORGANISM: Artificail sequence
W--> 76 <220> FEATURE:
W--> 76 <223> OTHER INFORMATION:
       76 <400> SEQUENCE: 7
       77 gggaaggatg gcgcacgctg                              20
       79 <210> SEQ ID NO: 8
       80 <211> LENGTH: 17
       81 <212> TYPE: DNA
C--> 82 <213> ORGANISM: Artificail sequence
W--> 84 <220> FEATURE:
W--> 84 <223> OTHER INFORMATION:
       84 <400> SEQUENCE: 8
       85 cgcgtgcgac cctcttg                                17
       87 <210> SEQ ID NO: 9
       88 <211> LENGTH: 17
       89 <212> TYPE: DNA
C--> 90 <213> ORGANISM: Artificail sequence
W--> 92 <220> FEATURE:
W--> 92 <223> OTHER INFORMATION:
       92 <400> SEQUENCE: 9
       93 taccgcgtgc gaccctc                                17
       95 <210> SEQ ID NO: 10
       96 <211> LENGTH: 17
       97 <212> TYPE: DNA
C--> 98 <213> ORGANISM: Artificail sequence
W--> 100 <220> FEATURE:
W--> 100 <223> OTHER INFORMATION:
      100 <400> SEQUENCE: 10
      101 tcctaccgcg tgcgacc                                17
      103 <210> SEQ ID NO: 11
```

RAW SEQUENCE LISTING   DATE: 02/07/2002
PATENT APPLICATION: US/10/053,645   ·TIME: 12:30:12

Input Set : A:\SEQ LISTING OF 10412-022.TXT
Output Set: N:\CRF3\02072002\J053645.raw

```
        104 <211> LENGTH: 17
        105 <212> TYPE: DNA
C-->    106 <213> ORGANISM: Artificail sequence
W-->    108 <220> FEATURE:
W-->    108 <223> OTHER INFORMATION:
        108 <400> SEQUENCE: 11
        109 ccttcctacc gcgtgcg                                    17
        111 <210> SEQ ID NO: 12
        112 <211> LENGTH: 17
        113 <212> TYPE: DNA
C-->    114 <213> ORGANISM: Artificail sequence
W-->    116 <220> FEATURE:
W-->    116 <223> OTHER INFORMATION:
        116 <400> SEQUENCE: 12
        117 gacccttcct accgcgt                                    17
        119 <210> SEQ ID NO: 13
        120 <211> LENGTH: 17
        121 <212> TYPE: DNA
C-->    122 <213> ORGANISM: Artificail sequence
W-->    124 <220> FEATURE:
W-->    124 <223> OTHER INFORMATION:
        124 <400> SEQUENCE: 13
        125 ggagaccctt cctaccg                                    17
        127 <210> SEQ ID NO: 14
        128 <211> LENGTH: 15
        129 <212> TYPE: DNA
C-->    130 <213> ORGANISM: Artificail sequence
W-->    132 <220> FEATURE:
W-->    132 <223> OTHER INFORMATION:
        132 <400> SEQUENCE: 14
        133 gcggcggcag cgcgg                                      15
        135 <210> SEQ ID NO: 15
        136 <211> LENGTH: 15
        137 <212> TYPE: DNA
C-->    138 <213> ORGANISM: Artificail sequence
W-->    140 <220> FEATURE:
W-->    140 <223> OTHER INFORMATION:
        140 <400> SEQUENCE: 15
        141 cggcggggcg acgga                                      15
        143 <210> SEQ ID NO: 16
        144 <211> LENGTH: 16
        145 <212> TYPE: DNA
C-->    146 <213> ORGANISM: Artificail sequence
W-->    148 <220> FEATURE:
W-->    148 <223> OTHER INFORMATION:
        148 <400> SEQUENCE: 16
        149 cgggagcgcg gcgggc                                     16
        151 <210> SEQ ID NO: 17
        152 <211> LENGTH: 18
```

RAW SEQUENCE LISTING   DATE: 02/07/2002
PATENT APPLICATION: US/10/053,645   TIME: 12:30:12

Input Set : A:\SEQ LISTING OF 10412-022.TXT
Output Set: N:\CRF3\02072002\J053645.raw

```
       153 <212> TYPE: DNA
C--> 154 <213> ORGANISM: Artificail sequence
W--> 156 <220> FEATURE:
W--> 156 <223> OTHER INFORMATION:
       156 <400> SEQUENCE: 17
       157 tctcccagcg tgcgccat                                              18
       159 <210> SEQ ID NO: 18
       160 <211> LENGTH: 18
       161 <212> TYPE: DNA
C--> 162 <213> ORGANISM: Artificail sequence
W--> 164 <220> FEATURE:
W--> 164 <223> OTHER INFORMATION:
       164 <400> SEQUENCE: 18
       165 tgcactcacg ctcggcct                                             18
       167 <210> SEQ ID NO: 19
       168 <211> LENGTH: 106
       169 <212> TYPE: DNA
C--> 170 <213> ORGANISM: Artificail sequence
W--> 172 <220> FEATURE:
W--> 172 <223> OTHER INFORMATION:
       172 <400> SEQUENCE: 19
       173 gcgcccgccc ctccgcgccg cctgcccgcc cgcccgccgc gctcccgccc gccgctctcc 60
       174 ccttattgtt aaaaacatgt tagaagcaat gaatgtatat aaaagc                106
       176 <210> SEQ ID NO: 20
       177 <211> LENGTH: 717
       178 <212> TYPE: DNA
       179 <213> ORGANISM: Homo Sapiens
       181 <220> FEATURE:
       182 <221> NAME/KEY: CDS
       183 <222> LOCATION: (1)...(717)
       185 <400> SEQUENCE: 20
       186 atg gcg cac gct ggg aga acg ggg tac gac aac cgg gag ata gtg atg  48
       187 Met Ala His Ala Gly Arg Thr Gly Tyr Asp Asn Arg Glu Ile Val Met
       188 1               5                   10                  15
       190 aag tac atc cat tat aag ctg tcg cag agg ggc tac gag tgg gat gcg  96
       191 Lys Tyr Ile His Tyr Lys Leu Ser Gln Arg Gly Tyr Glu Trp Asp Ala
       192             20                  25                  30
       194 gga gat gtg ggc gcc gcg ccc ccg ggg gcc gcc ccc gca ccg ggc atc  144
       195 Gly Asp Val Gly Ala Ala Pro Pro Gly Ala Ala Pro Ala Pro Gly Ile
       196             35                  40                  45
       198 ttc tcc tcc cag ccc ggg cac acg ccc cat cca gcc gca tcc cgc gac  192
       199 Phe Ser Ser Gln Pro Gly His Thr Pro His Pro Ala Ala Ser Arg Asp
       200         50                  55                  60
       202 ccg gtc gcc agg acc tcg ccg ctg cag acc ccg gct gcc ccc ggc gcc  240
       203 Pro Val Ala Arg Thr Ser Pro Leu Gln Thr Pro Ala Ala Pro Gly Ala
       204 65                  70                  75                  80
       206 gcc gcg ggg cct gcg ctc agc ccg gtg cca cct gtg gtc cac ctg gcc  288
       207 Ala Ala Gly Pro Ala Leu Ser Pro Val Pro Pro Val Val His Leu Ala
       208             85                  90                  95
```

The types of errors shown exist throughout the sequence listing. Please check subsequent sequences for similar errors.

```
210 ctc cgc caa gcc ggc gac gac ttc tcc cgc cgc tac cgc ggc gac ttc   336
211 Leu Arg Gln Ala Gly Asp Asp Phe Ser Arg Arg Tyr Arg Gly Asp Phe
212         100             105                 110
214 gcc gag atg tcc agc cag ctg cac ctg acg ccc ttc acc gcg cgg gga   384
215 Ala Glu Met Ser Ser Gln Leu His Leu Thr Pro Phe Thr Ala Arg Gly
216         115             120                 125
218 cgc ttt gcc acg gtg gtg gag gag ctc ttc agg gac ggg gtg aac tgg   432
219 Arg Phe Ala Thr Val Val Glu Glu Leu Phe Arg Asp Gly Val Asn Trp
220         130             135                 140
222 ggg agg att gtg gcc ttc ttt gag ttc ggt ggg gtc atg tgt gtg gag   480
223 Gly Arg Ile Val Ala Phe Phe Glu Phe Gly Gly Val Met Cys Val Glu
224 145             150                 155                 160
226 agc gtc aac cgg gag atg tcg ccc ctg gtg gac aac atc gcc ctg tgg   528
227 Ser Val Asn Arg Glu Met Ser Pro Leu Val Asp Asn Ile Ala Leu Trp
228         165             170                 175
230 atg act gag tac ctg aac cgg cac ctg cac acc tgg atc cag gat aac   576
231 Met Thr Glu Tyr Leu Asn Arg His Leu His Thr Trp Ile Gln Asp Asn
232         180             185                 190
234 gga ggc tgg gat gcc ttt gtg gaa ctg tac ggc ccc agc atg cgg cct   624
235 Gly Gly Trp Asp Ala Phe Val Glu Leu Tyr Gly Pro Ser Met Arg Pro
236         195             200                 205
238 ctg ttt gat ttc tcc tgg ctg tct ctg aag act ctg ctc agt ttg gcc   672
239 Leu Phe Asp Phe Ser Trp Leu Ser Leu Lys Thr Leu Leu Ser Leu Ala
240         210             215                 220
242 ctg gtg gga gct tgc atc acc ctg ggt gcc tat ctg agc cac aag        717
243 Leu Val Gly Ala Cys Ile Thr Leu Gly Ala Tyr Leu Ser His Lys
244 225             230                 235
248 <210> SEQ ID NO: 21
249 <211> LENGTH: 239
250 <212> TYPE: PRT
251 <213> ORGANISM: Homo Sapiens
253 <400> SEQUENCE: 21
254 Met Ala His Ala Gly Arg Thr Gly Tyr Asp Asn Arg Glu Ile Val Met
255  1               5                   10                  15
256 Lys Tyr Ile His Tyr Lys Leu Ser Gln Arg Gly Tyr Glu Trp Asp Ala
257         20              25                  30
258 Gly Asp Val Gly Ala Ala Pro Pro Gly Ala Ala Pro Ala Pro Gly Ile
259         35              40                  45
260 Phe Ser Ser Gln Pro Gly His Thr Pro His Pro Ala Ala Ser Arg Asp
261         50              55                  60
262 Pro Val Ala Arg Thr Ser Pro Leu Gln Thr Pro Ala Ala Pro Gly Ala
263 65              70                  75                  80
264 Ala Ala Gly Pro Ala Leu Ser Pro Val Pro Pro Val Val His Leu Ala
265         85                  90                  95
266 Leu Arg Gln Ala Gly Asp Asp Phe Ser Arg Arg Tyr Arg Gly Asp Phe
267         100             105                 110
268 Ala Glu Met Ser Ser Gln Leu His Leu Thr Pro Phe Thr Ala Arg Gly
269         115             120                 125
270 Arg Phe Ala Thr Val Val Glu Glu Leu Phe Arg Asp Gly Val Asn Trp
```

VERIFICATION SUMMARY　　　　　　　DATE: 02/07/2002
PATENT APPLICATION:　US/10/053,645　　TIME: 12:30:13

Input Set : **A:\SEQ LISTING OF 10412-022.TXT**
Output Set: **N:\CRF3\02072002\J053645.raw**

```
L:13  M:270 C: Current Application Number differs, Replaced Current Application Number
L:26  M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:1
L:28  M:258 W: Mandatory Feature missing, <220> FEATURE:
L:28  M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:34  M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:2
L:36  M:258 W: Mandatory Feature missing, <220> FEATURE:
L:36  M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:42  M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:3
L:44  M:258 W: Mandatory Feature missing, <220> FEATURE:
L:44  M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:50  M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:4
L:52  M:258 W: Mandatory Feature missing, <220> FEATURE:
L:52  M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:58  M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:5
L:60  M:258 W: Mandatory Feature missing, <220> FEATURE:
L:60  M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:66  M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:6
L:68  M:258 W: Mandatory Feature missing, <220> FEATURE:
L:68  M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:74  M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:7
L:76  M:258 W: Mandatory Feature missing, <220> FEATURE:
L:76  M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:82  M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:8
L:84  M:258 W: Mandatory Feature missing, <220> FEATURE:
L:84  M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:90  M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:9
L:92  M:258 W: Mandatory Feature missing, <220> FEATURE:
L:92  M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:98  M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:10
L:100 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:100 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:106 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:11
L:108 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:108 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:114 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:12
L:116 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:116 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:122 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:13
L:124 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:124 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:130 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:14
L:132 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:132 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:138 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:15
L:140 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:140 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:146 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:16
L:148 M:258 W: Mandatory Feature missing, <220> FEATURE:
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VERIFICATION SUMMARY
PATENT APPLICATION: US/10/053,645

DATE: 02/07/2002
TIME: 12:30:13

Input Set : **A:\SEQ LISTING OF 10412-022.TXT**
Output Set: **N:\CRF3\02072002\J053645.raw**

```
L:148 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:154 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:17
L:156 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:156 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:162 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:18
L:164 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:164 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:170 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:19
L:172 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:172 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:386 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:24
L:388 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:388 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:394 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:25
L:396 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:396 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:402 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:26
L:404 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:404 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:410 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:27
L:412 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:412 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:418 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:28
L:420 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:420 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:426 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:29
L:428 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:428 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
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